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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=29; hr=12; min=54; sec=12; ms=945;]

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Application No: 10568422 Version No: 2.0

Input Set:

Output Set:

Started: 2010-01-15 10:28:01.076
Finished: 2010-01-15 10:28:09.492
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 416 ms
Total Warnings: 2
Total Errors: 23
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (33)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (56)

Input Set:

Output Set:

Started: 2010-01-15 10:28:01.076
Finished: 2010-01-15 10:28:09.492
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 416 ms
Total Warnings: 2
Total Errors: 23
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (81)
E 321	No. of Bases conflict, this line has no nucleotides SEQID (91)
W 213	Artificial or Unknown found in <213> in SEQ ID (92)
W 213	Artificial or Unknown found in <213> in SEQ ID (93)

aatactaata	aaaactatat	tgctggagaa	gctgttactg	ggcaaccaat	caaattgaaa	1320
tcacatacag	acggtagtt	tgagattaaa	ggtttggctt	atgcagtta	tgcgaatgca	1380
gagggtacag	cagtaactta	caaattaaaa	gaaacaaaag	caccagaagg	ttatgtatc	1440
cctgataaaag	aaatcgat	tacagtatca	caaacatctt	ataatacaca	accaactgac	1500
atcacggtt	atagtgc	tgcaacacct	gatacaatta	aaaacaacaa	acgtcctca	1560
atccctaata	ctgggttat	tggtacggct	atcttgc	ctatcggtgc	tgcgtgatg	1620
gctttgctg	ttaagggat	gaagcgtcgt	acaaaagata	ac		1662

<210> 2
 <211> 554
 <212> PRT
 <213> *Streptococcus agalactiae*

<400> 2															
Met	Lys	Leu	Ser	Lys	Lys	Leu	Leu	Phe	Ser	Ala	Ala	Val	Leu	Thr	Met
1		5				10						15			
Val	Ala	Gly	Ser	Thr	Val	Glu	Pro	Val	Ala	Gln	Phe	Ala	Thr	Gly	Met
					20			25				30			
Ser	Ile	Val	Arg	Ala	Ala	Glu	Val	Ser	Gln	Glu	Arg	Pro	Ala	Lys	Thr
						35		40			45				
Thr	Val	Asn	Ile	Tyr	Lys	Leu	Gln	Ala	Asp	Ser	Tyr	Lys	Ser	Glu	Ile
					50		55				60				
Thr	Ser	Asn	Gly	Gly	Ile	Glu	Asn	Lys	Asp	Gly	Glu	Val	Ile	Ser	Asn
					65		70			75		80			
Tyr	Ala	Lys	Leu	Gly	Asp	Asn	Val	Lys	Gly	Leu	Gln	Gly	Val	Gln	Phe
					85		90			95					
Lys	Arg	Tyr	Lys	Val	Lys	Thr	Asp	Ile	Ser	Val	Asp	Glu	Leu	Lys	Lys
					100		105			110					
Leu	Thr	Thr	Val	Glu	Ala	Ala	Asp	Ala	Lys	Val	Gly	Thr	Ile	Leu	Glu
					115		120			125					
Glu	Gly	Val	Ser	Leu	Pro	Gln	Lys	Thr	Asn	Ala	Gln	Gly	Leu	Val	Val
					130		135			140					
Asp	Ala	Leu	Asp	Ser	Lys	Ser	Asn	Val	Arg	Tyr	Leu	Tyr	Val	Glu	Asp
					145		150			155		160			
Leu	Lys	Asn	Ser	Pro	Ser	Asn	Ile	Thr	Lys	Ala	Tyr	Ala	Val	Pro	Phe
					165		170			175					
Val	Leu	Glu	Leu	Pro	Val	Ala	Asn	Ser	Thr	Gly	Thr	Gly	Phe	Leu	Ser
					180		185			190					
Glu	Ile	Asn	Ile	Tyr	Pro	Lys	Asn	Val	Val	Thr	Asp	Glu	Pro	Lys	Thr
					195		200			205					
Asp	Lys	Asp	Val	Lys	Lys	Leu	Gly	Gln	Asp	Asp	Ala	Gly	Tyr	Thr	Ile
					210		215			220					
Gly	Glu	Glu	Phe	Lys	Trp	Phe	Leu	Lys	Ser	Thr	Ile	Pro	Ala	Asn	Leu
					225		230			235		240			
Gly	Asp	Tyr	Glu	Lys	Phe	Glu	Ile	Thr	Asp	Lys	Phe	Ala	Asp	Gly	Leu
					245		250			255					
Thr	Tyr	Lys	Ser	Val	Gly	Lys	Ile	Lys	Ile	Gly	Ser	Lys	Thr	Leu	Asn
					260		265			270					
Arg	Asp	Glu	His	Tyr	Thr	Ile	Asp	Glu	Pro	Thr	Val	Asp	Asn	Gln	Asn
					275		280			285					
Thr	Leu	Lys	Ile	Thr	Phe	Lys	Pro	Glu	Lys	Phe	Lys	Glu	Ile	Ala	Glu
					290		295			300					
Leu	Leu	Lys	Gly	Met	Thr	Leu	Val	Lys	Asn	Gln	Asp	Ala	Leu	Asp	Lys
					305		310			315		320			
Ala	Thr	Ala	Asn	Thr	Asp	Asp	Ala	Ala	Phe	Leu	Glu	Ile	Pro	Val	Ala
					325		330			335					
Ser	Thr	Ile	Asn	Glu	Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr

340	345	350	
Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys			
355	360	365	
Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg			
370	375	380	
Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu			
385	390	395	400
Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala			
405	410	415	
Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val			
420	425	430	
Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu			
435	440	445	
Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala			
450	455	460	
Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile			
465	470	475	480
Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr			
485	490	495	
Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr			
500	505	510	
Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly			
515	520	525	
Thr Ala Ile Phe Val Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val			
530	535	540	
Lys Gly Met Lys Arg Arg Thr Lys Asp Asn			
545	550		

<210> 3
<211> 517
<212> PRT
<213> Streptococcus agalactiae

<400> 3			
Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr			
1	5	10	15
Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile Thr Ser Asn Gly Gly			
20	25	30	
Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly			
35	40	45	
Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val			
50	55	60	
Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu			
65	70	75	80
Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu			
85	90	95	
Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val Asp Ala Leu Asp Ser			
100	105	110	
Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro			
115	120	125	
Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro			
130	135	140	
Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr			
145	150	155	160
Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys			

165	170	175
Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys		
180	185	190
Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys		
195	200	205
Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val		
210	215	220
Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr		
225	230	235
240		
Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr		
245	250	255
Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly Met		
260	265	270
Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr		
275	280	285
Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn Glu		
290	295	300
Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr		
305	310	315
320		
Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro		
325	330	335
Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys Asp		
340	345	350
Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala		
355	360	365
Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn		
370	375	380
Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro Ile		
385	390	395
400		
Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala		
405	410	415
Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu		
420	425	430
Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile		
435	440	445
Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile		
450	455	460
Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys		
465	470	475
480		
Arg Pro Ser Ile Pro Asn Thr Gly Ile Gly Thr Ala Ile Phe Val		
485	490	495
Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val Lys Gly Met Lys Arg		
500	505	510
Arg Thr Lys Asp Asn		
515		

<210> 4
 <211> 525
 <212> PRT
 <213> Streptococcus agalactiae

<400> 4
 Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
 1 5 10 15
 Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
 20 25 30
 Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr

35	40	45
Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser	Tyr Lys Ser Glu Ile	
50	55	60
Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly	Glu Val Ile Ser Asn	
65	70	75
Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly	Leu Gln Gly Val Gln Phe	
85	90	95
Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp	Glu Leu Lys Lys	
100	105	110
Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val	Gly Thr Ile Leu Glu	
115	120	125
Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala	Gln Gly Leu Val Val	
130	135	140
Asp Ala Leu Asp Ser Lys Ser Asn Val Arg	Tyr Leu Tyr Val Glu Asp	
145	150	155
Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala	Tyr Ala Val Pro Phe	
165	170	175
Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly	Thr Gly Phe Leu Ser	
180	185	190
Glu Ile Asn Ile Tyr Pro Lys Asn Val Val	Thr Asp Glu Pro Lys Thr	
195	200	205
Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp	Ala Gly Tyr Thr Ile	
210	215	220
Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr	Ile Pro Ala Asn Leu	
225	230	235
Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys	Phe Ala Asp Gly Leu	
245	250	255
Thr Tyr Lys Ser Val Gly Lys Ile Gly Ser Lys	Thr Leu Asn	
260	265	270
Arg Asp Glu His Tyr Thr Ile Asp Glu Pro	Thr Val Asp Asn Gln Asn	
275	280	285
Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe	Lys Glu Ile Ala Glu	
290	295	300
Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln	Asp Ala Leu Asp Lys	
305	310	315
Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe	Leu Glu Ile Pro Val Ala	
325	330	335
Ser Thr Ile Asn Glu Lys Ala Val Leu Gly	Lys Ala Ile Glu Asn Thr	
340	345	350
Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys	Ala Asp Asn Pro Lys	
355	360	365
Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His	Thr Gly Gly Lys Arg	
370	375	380
Phe Val Lys Lys Asp Ser Thr Glu Thr Gln	Thr Leu Gly Gly Ala Glu	
385	390	395
Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val	Lys Trp Thr Asp Ala	
405	410	415
Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr	Ile Ala Gly Glu Ala Val	
420	425	430
Thr Gly Gln Pro Ile Lys Leu Lys Ser His	Thr Asp Gly Thr Phe Glu	
435	440	445
Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn	Ala Glu Gly Thr Ala	
450	455	460
Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro	Glu Gly Tyr Val Ile	
465	470	475
Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln	Thr Ser Tyr Asn Thr	
485	490	495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
 500 505 510
 Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly
 515 520 525

 <210> 5
 <211> 5
 <212> PRT
 <213> Streptococcus agalactiae

 <400> 5
 Ile Pro Asn Thr Gly
 1 5

 <210> 6
 <211> 520
 <212> PRT
 <213> Streptococcus agalactiae

 <400> 6
 Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
 1 5 10 15
 Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
 20 25 30
 Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
 35 40 45
 Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
 50 55 60
 Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
 65 70 75 80
 Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
 85 90 95
 Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
 100 105 110
 Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
 115 120 125
 Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
 130 135 140
 Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
 145 150 155 160
 Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
 165 170 175
 Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
 180 185 190
 Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
 195 200 205
 Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
 210 215 220
 Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
 225 230 235 240
 Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
 245 250 255
 Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
 260 265 270
 Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
 275 280 285
 Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu

290	295	300													
Leu	Leu	Lys	Gly	Met	Thr	Leu	Val	Lys	Asn	Gln	Asp	Ala	Leu	Asp	Lys
305						310					315				320
Ala	Thr	Ala	Asn	Thr	Asp	Asp	Ala	Ala	Phe	Leu	Glu	Ile	Pro	Val	Ala
									325	330				335	
Ser	Thr	Ile	Asn	Glu	Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr
								340	345						